

[illegible]

Chemistry: Dye-terminator RT, 94x of reads
 Assembly program: Phrap, Phrap assembly
 Assembly program: Phrap, Phrap assembly
 Consensus quality: 19181 bases at least Q40
 Consensus quality: 19159 bases at least Q30
 Consensus quality: 19159 bases at least Q20
 Insert size: 10197; sum-of-contigs
 Quality coverage: 8.5x in Q40 bases; sum-of-contigs

Overlapping Sequences:

1: RF5-82925 AL138797
 3: RF5-96365 UW6C:sc02271 AC099763, 72727-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

assembly, but they are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

All sequons were either double-stranded or single-stranded.

The electronically-disgusted sequence consists of both insert and

vector, in order to accurately represent the entire circular HAC.

Small fragments below a variable cutoff (approximately 400-800 bp)

are not included in the table. There are no significant remaining discrepancies

between the experimental and predicted values. Uniquely ordered

fragments are separated by double lines.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest

fingerprinting. Comparison of the experimentally derived digest

with the predicted digest confirms the sequence.

The electronically-disgusted sequence consists of both insert and

vector, in order to accurately represent the entire circular HAC.

Small fragments below a variable cutoff (approximately 400-800 bp)

are not included in the table. There are no significant remaining discrepancies

between the experimental and predicted values. Uniquely ordered

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vector, in order to accurately represent the entire circular HAC.

Small fragments below a variable cutoff (approximately 400-800 bp)

are not included in the table. There are no significant remaining discrepancies

between the experimental and predicted values. Uniquely ordered

fragments are separated by double lines.

3432	3369	3414	3370	4861	4963
761	<800	5158	5047	4230	4250
4142	4283	3809	3727	1367	1348
291	<800	1435	1490	5341	5276
387	3673	429	<800	1607	1607
5808	5419	7141	7077	5055	4963
731	<800	4553	4856	717	<800
6894	6952	1346	1326	5845	5875
5282	5419	3858	3727	10637	10818
2262	2231	5381	5410	5112	4963
1478	1430	443	<800	3656	3692
345	<800	2930	2885	13460	13440
3254	3369	5480	5410	447	<800
18	<800	1436	<800	1406	4250
3192	3059	2341	2079	1024	1013
3192	3059	6411	6307	1526	1607
522	<800	2574	2661	16171	16269
5580	5658	7245	7077	138	<800
902	912	2035	2079	171	<800
3475	3369	1235	1264	7820	7857
6779	6952	4452	4388	757	<800
2609	2559	2587	2661	1990	1897
624	640	263	2661	2185	2130
617	<800	86	<800	1454	1461
3253	3369	2087	2079	4370	4250
4262	4283	7747	7601	1631	1607
674	<800	548	<800	3421	3450
50	<800	6363	6307	9	<800
5659	5658	69	<800	979	1013
3884	3673	1554	1613	177	<800
1045	1046	1774	1726	7	<800
1222	1229	3509	3471	1848	1897
1046	1046	1614	1613	6310	6310
1570	1536	15635	15635	2599	2652
301	3059	2144	2261	136	1348

COMMENT

On May 30, 2002 this sequence version replaced gi:17017668.

----- Genome Center
 Center: University of Washington Genome Center
 Web site: <http://www.genome.washington.edu>
 Contact: usgshsu@u.washington.edu
 Drifting Contact:
 Drifting Project Information
 Center Project name: chr1

Center clone name: RP5-963M5 (sc0227)

Sequencing vector: plasmid; 48x of reads
 Sequencing strategy: L08752, 52x of reads
 Chemistry: Big Dye Terminator 3.1
 Chemistry: Big Dye Terminator 3.1
 Assembly program: Phrap; version 0.950319
 Consensus quality: 9972 bases at least Q40
 Consensus quality: 9972 bases at least Q40
 Consensus quality: 9976 bases at least Q40
 Insert size: 9680; sum-of-contigs
 Quality coverage: 7.1x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5: Mapping in progress
 5: Mapping in progress (NM00300329) AGL05932

Sequence Quality Assessment:
 This entry has been manually checked with sequence quality
 information from the Big Dye Phrap assembly.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error per 10,000 bases.
 Base-by-base quality values are not generally visible from the
 Genbank flat file format but are available as part
 of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
 all regions were either double-stranded or sequenced with an
 independent primer.
 quality > 30; an attempt was made to resolve all sequencing
 problems, such as compressions and repeats; all regions were
 covered by at least one plus/minus subclone or more than one RFLP
 probe.

Sequence Validation:
 This sequence was validated by Multiple Complete Digest
 fingerprinting. Comparison of the experimentally derived digest
 fragments with sequence-predicted fragments is given below.
 The electronically-digested sequence consists of both insert and
 vector. The vector sequence is indicated by a dashed line.
 Small fragments below a variable cutoff (approximately 400-800 bp)
 are not resolved in the fingerprint and hence do not appear
 in the predicted values.
 Between the experimental and predicted values, uniquely ordered
 fragments are separated by dashed lines.

SeqlenMap	ExpPrint	SeqlenMap	ExpPrint	SeqlenMap	ExpPrint
8218	8256	3868	3816	9681	9741
218	2152	445	<800	5071	5776
8065	8256	512	<800	5119	5161
495	<800	781	2786	3984	3908
106	<800	1247	1215	1045	1030
7165	7251	4695	4684	1222	1202

FEATURES

source
 1. 59880
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 /db_xref="taxon:9606"
 /db_xref="taxon:9606"

69	<800	3373	3395	993	1030
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1774	1747	9	<800	3010	3012
3509	3513	879	991	21	<800
1674	1747	177	<800	1638	1637
15633	15657	7	<800	750	757
2149	2152	1848	1871	3612	3599
2439	2458	6207	6240	456	<800
1743	1747	2559	2614	198	<800
4956	4956	1346	1369	898	902
807	807	1004	991	31	<800
2289	2295	543	<800	1044	1030
4347	4235	1893	1871	11903	11821
1336	1346	10227	10300	192	<800
1096	1105	510	930	270	<800
5165	5125	1156	1143	4469	4454
3234	3219	3009	2991	2425	2412
1762	12605	629	6240	7642	7795
1160	1146	8937	8886	111	<800
286	<800	2764	2786	1019	1030
1446	1415	2965	2991	4355	4335
2883	2905	2050	2050	4948	4908
2114	2152	985	<800	311	<800
60	<800	4282	4220	4904	4908
1797	1747	3257	3251	1704	1637
464	<800	5452	5378	6043	6069
100	3059	910	1871	817	824
364	<800	793	801	884	902
6320	6286	9342	9358	667	<800
2899	2905	1729	1710	3519	3495
		5916	5907	2396	2412
		3149	3159	2317	2326
		2159	2202	13269	13278
		2758	2786		

Location/Qualifiers

1. 59880
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /db_xref="taxon:9606"


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misc_feature      1792..3774
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misc_feature
/note="assembly_name:Contig12"
5195..5617
/note="assembly_name:Contig13"
misc_feature
/note="assembly_name:Contig14"
18257..47595
/note="assembly_name:Contig15"
48097..81693
/note="assembly_name:Contig16"
81991..121154
/note="assembly_name:Contig17"
121255..337637
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/note="assembly_name:Contig18"
378477..254633
misc_feature
/note="assembly_name:Contig19"
70197 a 56746 c 55884 g 71184 t 922 others
ORIGIN
Query Match      23.0%; Score 298.2; db 2; Length 254933;
Best Local Similarity 82.4%; Pred. No. 2,6e-70;
Matches 342; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 377 AGCTTTCACAGTGGTGAACCTTGTGCGCAATGTCGAACTGAGTGAGTGTG 436
Db 84149 TTTT|||||TTTT|||||TTTT|||||TTTT|||||TTTT|||||TTTT|||||
QY 437 GCCAGAGTGGGAATGATGATGATCTCTCGATTTGGGAATGACATGCC 496
Db 84089 GCGAGAGTGGGAGAGATGATGATCTCTCGATTTGGGAATGACATGCC 44030
QY 497 CACCAAGATTATGAGAGATGTCGCGCCGACGACGATGATTCGATTTGCCATA 556
Db 84029 CACCGAGGCTTTGGGAGAGATGTCGCGCCGACGACGATGATTTGCCATA 83970
QY 557 CCGAGTCTCTTTTCATAAAGCTGATATTTTCAGGAGGAGTACTACTA 616
Db 83969 CAGATGCTCTCTTTTCATAAAGCTGATATTTTCAGGAGGAGTACTACTA 83910
QY 617 TTGTGTTATTTGGGACCTTCCCAATATGAGAAATGGCATGGCTCTTACA 676
Db 83909 TTATGTTATTTGGGACCTTCCCAATATGAGAAATGGCATGGCTCTTACA 83850
QY 677 ACATGTTGAAAGACATGTTGATCTATCTCCAGTCCCAATATATGATGCCAGAGA 736
Db 83849 ACATGTTGAAAGACATGTTGATCTATCTCCAGTCCCAATATATGATGCCAGAGA 83790
QY 737 ACACAGATGATCTATGATGATTTTATGAGAAATGGCATGGCTCTTACA 791
Db 83789 ACACAGATGATCTATGATGATTTTATGAGAAATGGCATGGCTCTTACA 83735

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Search completed: September 12, 2003, 14:10:54
 Job time : 5035 secs

OE	acetylgl
OE	(NeuAc-
OE	(ST6Gal
GN	SIAT7D
OS	Homo sa
OC	Eukaryo

[illegible]

CC	entity or send
CC	EMBL; A
CC	EMBL; A
CC	EMBL; A
DR	EMBL; A
DR	EMBL; A
DR	EMBL; A
DR	EMBL; A

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230	TCCTGG	-----TTGGCGCTCTTAATAGAGAGGAAATTCCTGCTCTCAAT	27
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339	TCCTGG		136
340	TCCTGG		137
341	TCCTGG		138


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Query Match: 5.7% Indels: 45
DB: 2 Gaps: 4

US-09-714-936-218 (1-1294) x US-08-446-875-10 (1-375)

QY 283 TTTCAGACCTGTCACAGATGGATGACATCTCTCCACACAGAGGCGCCCTTCA 342
DB 102 PHESETYFROALPROMETPheluaaspserPhealystPAlaagileay 121
QY 343 ACTACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 384
QY 122 GUPLHVALProPheGlyLeuLysLeuLysLeuLysLeuLysLeuLysLeuLys 41
QY 385 -----CACTGACCTGACCTTCCGC 408
DB 142 ValtrLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 361
QY 409 KMGATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 468
DB 162 ILevalGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 181
QY 469 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
DB 122 AsplValValValValValValValValValValValValValValValVal 201
QY 589 TATTTCAGACGACATGACATGACATGACATGACATGACATGACATGACATGACAT 645
DB 219 GlnTYGlnAlaGAspSerLeuPheValLeuAlaLysLysLysLysLysLys 705
QY 646 ATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 705
DB 239 LeuLys -----TyrLeuValTyrLysLysLysLysLysLysLysLys 240
QY 705 CGAGATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 765
DB 241 -----TyrLeuValTyrLysLysLysLysLysLysLysLysLysLys 255
QY 765 AAC 768
DB 255 Lys 256

RESULTS
US-09-714-936-218 (1-1294) x US-08-102-3850-10 (1-375)

QY 283 TTTCAGACCTGTCACAGATGGATGACATCTCTCCACACAGAGGCGCCCTTCA 342
DB 102 PHESETYFROALPROMETPheluaaspserPhealystPAlaagileay 121
QY 343 ACTACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 384
QY 122 GUPLHVALProPheGlyLeuLysLeuLysLeuLysLeuLysLeuLysLeuLys 41
QY 385 -----CACTGACCTGACCTTCCGC 408
DB 142 ValtrLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 361
QY 409 KMGATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 468
DB 162 ILevalGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 181
QY 469 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
DB 122 AsplValValValValValValValValValValValValValValValVal 201
QY 589 TATTTCAGACGACATGACATGACATGACATGACATGACATGACATGACATGACAT 645
DB 219 GlnTYGlnAlaGAspSerLeuPheValLeuAlaLysLysLysLysLysLys 705
QY 646 ATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 705
DB 239 LeuLys -----TyrLeuValTyrLysLysLysLysLysLysLysLys 240
QY 705 CGAGATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 765
DB 241 -----TyrLeuValTyrLysLysLysLysLysLysLysLysLysLys 255
QY 765 AAC 768
DB 255 Lys 256

RESULTS
US-09-446-875-15

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RESULTS 15
 US-09-446-875-15

Sequence 10, Application US/0810285G

Patent No. 5822200

APPLICANT: Paulson, James C.

APPLICANT: Wen, Xiaohong

APPLICANT: Wen, Xiaohong

APPLICANT: Gullerstein, William

APPLICANT: Kelm, George

APPLICANT: Burlingame, Anna T.

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases

CORRESPONDENCE ADDRESS:

ADDRESSER: Oppenheimer Wolff & Donnelly LLP

STREET: 209 Century Park East, 38th Floor

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90067

COMMENTS: AVAILABLE FORM:

MEDIA: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

VERSION: 1.0, Version #1.25

CURRENT APPLICATION DATA:

[illegible]

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[illegible]


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RESUME 15
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XX ID ABUS5203 standard; Protein: 210 kDa.
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XX Human secreted/transmembrane protein, PRO177.
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XX Human; secreted protein; transmembrane protein; PRO;
XX antiarthritic; villous; tumor necrosis factor-alpha;
XX tumor; adrenal tumor; lung tumor; liver tumor;
XX prostate tumor; rectal tumor; cervical tumor; liver tumor;
XX bone disorder; cartilage disorder; arthritis; sports injury.
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Search completed: September 12, 2003, 16:36:28
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Search completed: September 12, 2003, 16:37:38
 Job time : 47 secs

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ow nucleic - protein search, using frame_plus_n2p model

Run on: September 12, 2003, 16:37:44 ; Search time 52 Seconds
(without alignments)
7261.949 Million cell updates/sec

Title: US-09-714-936-218

Perfect score: 2383
Sequence: 1 ccggaatttcgggtgacg.....tttctctctctctctctctt 1294

Scoring table: BLOSUM62

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 1083872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 40 summaries

Command line parameters:

[illegible]

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- 2: /csm2_6/pdatata/pubsub/US96_NRW_RUN pep.
- 3: /csm2_6/pdatata/pubsub/US96_NRW_RUN pep.
- 4: /csm2_6/pdatata/pubsub/US96_NRW_PUB pep.
- 5: /csm2_6/pdatata/pubsub/US96_NRW_PUB pep.
- 6: /csm2_6/pdatata/pubsub/US96_NRW_PUB pep.
- 7: /csm2_6/pdatata/pubsub/US96_NRW_PUB pep.
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- 20: /csm2_6/pdatata/pubsub/US96_NRW_PUB pep.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
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[illegible]

ALIGNMENTS

RESULT 1-
19-672-536
APPLICANT: Baker, Kevin P.
AFFICANT: APPLICANT: Desnoyers, LaC
APPLICANT: APPLICANT: Godard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, William D.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watkinson, Colin K.
APPLICANT: APPLICANT: Zhang, Feilai
APPLICANT: APPLICANT: Zhang, Feilai
TITLE OF INVENTION: SECURED AND TRANSMITTER
FILE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/04/199,672
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 05/016,052,586
PRIOR APPLICATION NUMBER: 05/016,052,586
PRIOR APPLICATION NUMBER: 05/015,963

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1 PRIOR FILING DATE: 1997-09-18
2 PRIOR APPLICATION NUMBER: 60/059286
3 PRIOR FILING DATE: 1997-09-18
4 PRIOR APPLICATION NUMBER: 60/062230
5 PRIOR FILING DATE: 1997-10-17
6 PRIOR APPLICATION NUMBER: 60/063120
7 PRIOR FILING DATE: 1997-10-20
8 PRIOR APPLICATION NUMBER: 60/063121
9 PRIOR FILING DATE: 1997-10-20
10 PRIOR APPLICATION NUMBER: 60/063406
11 PRIOR FILING DATE: 1997-10-21
12 PRIOR APPLICATION NUMBER: 60/063540
13 PRIOR FILING DATE: 1997-10-21
14 PRIOR APPLICATION NUMBER: 60/063541
15 PRIOR FILING DATE: 1997-10-28
16 PRIOR APPLICATION NUMBER: 60/063544
17 PRIOR APPLICATION NUMBER: 60/063544
18 Remaining Prior Application data removed - See File Wrapper or PALM.
19 SEQ ID NO 316
20 SEQ ID NO 317
21 TYPE: PRT
22 ORGANISM: Homo Sapien
23 US-10-159-672-536
24 Alignment Scores:
25 Pred. No.: 1,036-101
26 Percent Similarity: 99.52%
27 Best Local Similarity: 99.52%
28 Mismatches: 1
29 Gaps: 0
30 DB:

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QY 226 TCTCTGCTGTGCTGCTGTGTAATGAAGTAATTCCTACTACTACAGCTTT 285
DB 21 PHLEALVALVALYALYGLVALHAGLVLAASERPHLEALVALLEALYCYSPHE 40
QY 286 GACACACTGCTGCAAGTGTGATCACTTCTTACACAGGCGCCCTTGACT 445
DB 41 GYGLYGLYGLYVALYGLYPLERPHSERCTTGTGTATGATGATGATGAT 60
QY 346 CATATGATGATCAATGAATGAGACAGAGCCCTTGATGATGATGATGAT 405
DB 61 HAAVGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 80
QY 406 GCATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 65
DB 81 ALALVALSERANSEGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 100
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DB 101 SERCTCYSLERTPARGMETANALALPHROTHLYGLYGLYGLYGLYGLY 120
QY 526 CAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 385
DB 121 ASYPTNTRMETILYALYVALSERVALSERVALSERVALSERVALSERVAL 140
QY 586 GATATATTTTCACAGACAGAGATGATGATGATGATGATGATGATGATG 445
DB 141 ASYPTNTRMETILYALYVALSERVALSERVALSERVALSERVALSERVAL 160
QY 646 ATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
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QY 706 CCATATGCCCAATPACATGATGATGATGATGATGATGATGATGATGAT 745
DB 21 PHLEALVALVALYALYGLVALHAGLVLAASERPHLEALVALLEALYCYSPHE 40

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QY 766 AGACACCAATCTGACACGAC 786
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RESULT 2
US-10-187-749-536
1 Sequence 536, Application US/10/187/49
2 Title of Invention: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
3 ACID SEQUENCES ENCODING THE SAME
4 GENERAL INFORMATION:
5 APPLICANT: Baker, Kevin P.
6 APPLICANT: Chen, Jian
7 APPLICANT: Chou, Yung-Chieh
8 APPLICANT: Goddard, Audrey
9 APPLICANT: Godowski, Paul J.
10 APPLICANT: Han, Joon-Gook
11 APPLICANT: Pan, Jing/Austin L.
12 APPLICANT: Smith, Victoria
13 APPLICANT: Smith, Victoria
14 APPLICANT: Smith, Victoria
15 APPLICANT: Zhang, Zemin
16 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
17 ACID SEQUENCES ENCODING THE SAME
18 FILING DATE: 2000-07-01
19 CURRENT APPLICATION NUMBER: US/10/187/49
20 PRIOR FILING DATE: 2000-07-01
21 PRIOR APPLICATION NUMBER: 60/059283
22 PRIOR FILING DATE: 2000-01-15
23 PRIOR APPLICATION NUMBER: 60/059283
24 PRIOR FILING DATE: 1997-09-18
25 PRIOR APPLICATION NUMBER: 60/059286
26 PRIOR FILING DATE: 1997-09-18
27 PRIOR APPLICATION NUMBER: 60/062250
28 PRIOR FILING DATE: 1997-10-21
29 PRIOR APPLICATION NUMBER: 60/063120
30 PRIOR FILING DATE: 1997-10-24
31 PRIOR APPLICATION NUMBER: 60/063121
32 PRIOR APPLICATION NUMBER: 60/063486
33 PRIOR FILING DATE: 1997-10-21
34 PRIOR APPLICATION NUMBER: 60/063540
35 PRIOR FILING DATE: 1997-10-28
36 PRIOR APPLICATION NUMBER: 60/063541
37 PRIOR FILING DATE: 1997-10-28
38 PRIOR APPLICATION NUMBER: 60/063544
39 Remaining Prior Application data removed - See File Wrapper or PALM.
40 NUMBER OF SEQ ID NOS: 612
41 SEQ ID NO 316
42 SEQ ID NO 317
43 TYPE: PRT
44 ORGANISM: Homo Sapien
45 US-10-187-749-536

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Alignment Scores:
Seq. No.: 1,036-101
Score: 1095.00
Percent Similarity: 99.52%
Best Local Similarity: 99.52%
Mismatches: 0
Gaps: 0
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DB 1 METALCYSTEINELYALYGLYSERYVALILEALVALSERPHLEALALAPHELE 20
QY 226 TCTCTGCTGTGCTGCTGTGTAATGAAGTAATTCCTACTACTACAGCTTT 285
DB 21 PHLEALVALVALYALYGLVALHAGLVLAASERPHLEALVALLEALYCYSPHE 40

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Db 744 GGCCTGGTGTGCCCAATGGAGCATGTGCCTCTCCGGCCGCGATCGGCAATT 803
 Qy 754 GTCGAGTCTTACAGAGATGATGATGATGATGATGATGATGATGATGATGAT 794
 Db 804 GAGCAGCTCTTCGGGGTGCAGCGCGAGGACAGGAGAA 844

RESULT 4
 US-08-446-875-15
 : Sequence 15 Application US/08446875
 : Patent No. 5851
 : GENERAL INFORMATION:
 : APPLICANT: Paulson, James C.
 : APPLICANT: Ben, Xishoung
 : APPLICANT: Paulson, Brian Duane
 : APPLICANT: Gillespie, William
 : APPLICANT: Kelm, Serge
 : APPLICANT: Bulliguesse, Alain
 : APPLICANT: Medzhidzsky, Katalin
 : TITLE OF INVENTION: Compositions and Methods for the
 : IDENTIFICATION and Synthesis of Sialyltransferases
 : NAME OF INVENTOR: Identification and Synthesis of Sialyltransferases
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Poma, Smith, Lande & Rose
 : STREET: 2025 Century Park East, Suite 3800
 : CITY: Los Angeles
 : STATE: CA
 : COUNTRY: USA
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION DATE: 08/446,875
 : FILING DATE: July 12, 1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION DATE: 08/102,385
 : FILING DATE: August 4, 1993
 : ATTORNEY/AGENT INFORMATION:
 : REGISTRATION NUMBER: 29,421
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (310) 277-1497
 : TELEFAX: (310) 277-1497
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : MOLECULE TYPE: cDNA
 : HYPOTHEICAL: NO
 : ORIGINATOR: Poma, Smith, Lande & Rose
 : ORIGIN TYPE: alter, subaxillary glands
 : FEATURE:
 : NAME/REF: CDS 1119
 : OTHER INFORMATION: /product- "porcine Gal Beta 1,3
 : OTHER INFORMATION: Gainac alpha 2,3 sialyltransferase"
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 : Matches 14; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
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 : Db 410 GGGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCT 459
 : Qy 449 TGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
 : Db 470 GCGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529
 : Qy 509 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 568
 : Db 530 TTAGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 589

Qy 569 TTTTCTTAAAAA 581
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 : Sequence 1 Application US/08446875
 : Patent No. 5851
 : GENERAL INFORMATION:
 : APPLICANT: Paulson, James C.
 : APPLICANT: Ben, Xishoung
 : APPLICANT: Paulson, Brian Duane
 : APPLICANT: Gillespie, William
 : APPLICANT: Kelm, Serge
 : APPLICANT: Bulliguesse, Alain
 : APPLICANT: Medzhidzsky, Katalin
 : TITLE OF INVENTION: Compositions and Methods for the
 : IDENTIFICATION and Synthesis of Sialyltransferases
 : NAME OF INVENTOR: Identification and Synthesis of Sialyltransferases
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Poma, Smith, Lande & Rose
 : STREET: 2025 Century Park East, Suite 3800
 : CITY: Los Angeles
 : STATE: CA
 : COUNTRY: USA
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION DATE: 08/446,875
 : FILING DATE: July 12, 1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION DATE: 08/102,385
 : FILING DATE: August 4, 1993
 : ATTORNEY/AGENT INFORMATION:
 : REGISTRATION NUMBER: 29,421
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (310) 277-1497
 : TELEFAX: (310) 277-1497
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : MOLECULE TYPE: cDNA
 : HYPOTHEICAL: NO
 : ORIGINATOR: Poma, Smith, Lande & Rose
 : ORIGIN TYPE: alter, subaxillary glands
 : FEATURE:
 : NAME/REF: CDS 1119
 : OTHER INFORMATION: /product- "porcine Gal Beta 1,3
 : OTHER INFORMATION: Gainac alpha 2,3 sialyltransferase"
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6 NAME/KEY: misc:feature
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8 OTHER INFORMATION: 5'regulatory region g35018 gene
9 FEATURE:
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12 OTHER INFORMATION: exon A g35018 gene
13 FEATURE:
14 NAME/KEY: exon
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16 OTHER INFORMATION: exon B g35018 gene
17 FEATURE:
18 NAME/KEY: exon
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20 OTHER INFORMATION: exon C g35018 gene
21 FEATURE:
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24 OTHER INFORMATION: exon D g35018 gene
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27 LOCATION: 23188..29502
28 OTHER INFORMATION: exon E g35018 gene
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32 OTHER INFORMATION: exon F g35018 gene
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51 LOCATION: 201188..201234
52 OTHER INFORMATION: exon S g35030 gene
53 FEATURE:
54 NAME/KEY: exon
55 LOCATION: 214676..214793
56 OTHER INFORMATION: exon T g35030 gene
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60 OTHER INFORMATION: exon U g35030 gene
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127 LOCATION: 240528..240569
128 OTHER INFORMATION: exon N117 complement g34872 gene
129 FEATURE:
130 NAME/KEY: exon
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132 OTHER INFORMATION: exon N1090 complement g34872 gene
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140 OTHER INFORMATION: exon N52 complement g34872 gene
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142 NAME/KEY: exon
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145 FEATURE:
146 NAME/KEY: exon

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LOCATION: 19163
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NAME/SET: allele

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Identical Similarity 4.7%;
Matches 90; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

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QY 1207 T 1207
DB 116909 T 116909

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Search completed: September 12, 2003, 15:04:52
Job time : 110 secs

Tang YF, Goodrich-Schulz, Liu C, Zhou F, Asanadi V, Zhang J, Zhao QH; Ren F, Xue AJ, Yang T, Wehrman T, Dzmanashvili R
NPI: 2007-59082/63.
NP-PDSB: ABP44885.

New isolated polynucleotide, useful in research, diagnostic or therapeutic applications, comprising at least one nucleotide sequence having an aberrant protein expression or biological activity

Claim 1: SEQ ID 204; 394pp; English.

The present invention relates to novel human coding sequences (AB039268-AB039508) and proteins (ARP4482-ARP45022). The sequences are used in research, diagnostic or therapeutic applications. They are hybridized probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense sequences. The polynucleotides are useful in diagnostics as expressed sequences of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used as immunological reagents for serological diagnosis and for detection of tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The polynucleotides and proteins are useful components of pharmaceutical compositions for treatment of diseases, e.g., hematopoietic disorders, protein expression or blood clotting activity, e.g., hemostatic disorders, central/peripheral nervous system diseases, mechanical and traumatic disorders, non-healing wounds, immune deficiencies and disorders, autoimmune disorders, allergic reactions and conditions, coagulation disorders, or cancer. The polynucleotide sequences of the invention were assembled from cDNAs isolated mainly by sequencing by hybridization, and some of them were obtained by other methods. The sequences of the printed specification, but was obtained in electronic form directly from NPIQ at file:wpio.int/pub/published_pc_sequences.

Sequence 1394, BP: 320 A: 313 C: 313 G: 349 T: 0 other;

[illegible]

DE Human DNA encoding PRO polypeptide sequence #268.

XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;


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PR 17-AUG-1998; 98US-086766P.
PR 17-AUG-1998; 98US-086807P.
PR 17-AUG-1998; 98US-086857P.
PR 17-AUG-1998; 98US-086897P.
PR 18-AUG-1998; 98US-086949P.
PR 18-AUG-1998; 98US-086999P.
PR 18-AUG-1998; 98US-087022P.
PR 18-AUG-1998; 98US-087052P.
PR 26-AUG-1998; 98US-087452P.
PR 26-AUG-1998; 98US-087452P.
PR 26-AUG-1998; 98US-087452P.
PR 26-AUG-1998; 98US-087452P.
PR 26-AUG-1998; 98US-087452P.
PR 26-AUG-1998; 98US-087452P.
PR 26-AUG-1998; 98US-087452P.
PR 26-AUG-1998; 98US-087452P.
PR 01-SEP-1998; 98US-087974P.
PR 01-SEP-1998; 98US-088110P.
PR 01-SEP-1998; 98US-088121P.
PR 02-SEP-1998; 98US-088403P.
PR 02-SEP-1998; 98US-088403P.
PR 02-SEP-1998; 98US-088417P.
PR 09-SEP-1998; 98US-089402P.
PR 10-SEP-1998; 98US-089414P.

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QY 44 TGGATCTGGGAAGTGGCTGGAGAGCTCTCCCTGGTGGACAGCTCCAGCTCCGC 103
DB 1 TGGATCTGGGAAGTGGCTGGAGAGCTCTCCCTGGTGGACAGCTCCAGCTCCGC 60
QY 104 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 163
DB 61 CAGAGCTGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 164 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 223
DB 121 CAGAGCTGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 224 TTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 283
DB 181 TTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 284 TGGAGAGCTCTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 343
DB 241 TGGAGAGCTCTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 344 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 403
DB 301 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 360
QY 404 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 463
DB 361 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 420
QY 464 GATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 523
DB 421 GATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 524 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 583
DB 481 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 540
QY 584 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 643
DB 541 CAGAGCTGGCTCTGAGAGAAAGTGTGTGATGTGTGGAGTTCATAGCAGCTGCC 600
QY 644 ATATAGAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 703
DB 601 ATATAGAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
QY 704 ATATAGAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 763
DB 661 ATATAGAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720

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QY 764 TTAGAGAGAGAGCTGGAGAGAC 788
 DB 721 TTAGAGAGAGAGCTGGAGAGAC 745
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 ID ASB98922 standard; cDNA; 1106 BP.
 XX ASB98922;
 XX ASB98922;
 DT 20-MAY-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO177 cDNA.
 XX Human, secreted protein; transmembrane protein; cytosolic;
 XX gene therapy; T-Agona6; Alpha; chondrocyte stimulator; tumour;
 XX prostate tumour; rectal tumour; cervical tumour; liver tumour;
 XX gene; ss.
 OS Homo sapiens.
 XX OS0303036157-Al.
 PD 20-FEB-2002; 2002US-0186769.
 XX 02-JUL-2002; 2002US-0186769.
 PR 16-SEP-1998; 98RO-US19330.
 PR 07-OCT-1998; 98RO-US21141.
 PR 08-MAR-1999; 98RO-US20528.
 PR 14-MAY-1999; 98RO-US10733.
 PR 02-JUN-1999; 98RO-US12252.
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 PR 01-DEC-1999; 98RO-US28301.
 PR 30-DEC-1999; 98RO-US31274.
 PR 05-JAN-2000; 2000RO-US00219.
 PR 18-FEB-2000; 2000RO-US04341.
 PR 22-FEB-2000; 2000RO-US04414.
 PR 24-FEB-2000; 2000RO-US05004.
 PR 01-MAR-2000; 2000RO-US05601.
 PR 15-MAR-2000; 2000RO-US06884.
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 PR 02-JUN-2000; 2000RO-US15264.
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 PR 08-NOV-2000; 2000RO-US30952.
 PR 30-DEC-2000; 2000RO-US34559.
 PR 28-FEB-2001; 2001RO-US06520.
 PR 01-JUN-2001; 2001RO-US17800.
 PR 29-AUG-2001; 2001RO-US21735.
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 PR 18-SEP-1999; 97US-052966P.
 PR 17-OCT-1999; 97US-062250P.
 PR 21-OCT-1997; 97US-063486P.
 PR 24-OCT-1997; 97US-063121P.
 PR 28-OCT-1997; 97US-063540P.
 PR 28-OCT-1997; 97US-063541P.
 PR 28-OCT-1997; 97US-063544P.

PE Claim 2; Fig 535; 706pp; English.

XX The invention discloses human nucleic acids encoding secreted and
 XX transmembrane (PRO) polypeptides. Also disclosed is an antibody that
 CC specifically binds to the PRO polypeptide, a method for stimulating the
 CC proliferation of chondrocyte cells by contacting the cells with the antibody
 CC contacting the blood or a PRO polypeptide, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells by contacting the
 CC cells with a PRO polypeptide, a method for detecting the presence of a
 CC PRO nucleotide sequence, the nucleic acid sequences are useful as probes,
 CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
 CC identifying polymorphic variant techniques and in gene therapy
 CC (e.g., for repair of defective genes). The PRO polypeptides are useful
 CC as molecular weight markers for protein electrophoresis purposes, for
 CC chromosome identification, as chromosome markers, as therapeutic agents,
 CC stimulating the proliferation or differentiation of chondrocytes and
 CC detecting the presence of a tumour. The PRO polypeptides and nucleic
 CC acids are useful for diagnosing and prognostically for tissue typing. The sequences
 CC disclosed in US45780-9 are useful for identifying the presence of a PRO
 CC polypeptides of the invention.

XX Sequence 1106 BP, 325 A; 226 C; 260 G; 295 T; 0 other;

Query Match
 Best Local Similarity 57.44; Score 743.4; DB 25; Length 1106;
 Matches 744; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGATCTGGGAAATGGGCTGGAGAGTCTGGCTGGCTGAGTACAGCTCCAGCTTCCCTC 103
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 QY 104 CCGAGACTCCCTCCACCCAGCGCGCGCCCTCTCTGGTGGAGAGAGGCGCGCGGAGCG 163
 CC CCGAGACTCCCTCCACCCAGCGCGCGCCCTCTCTGGTGGAGAGAGGCGCGCGGAGCG 120
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 DB 301 CTCACTATGATCACTAATGTGTGAGACACAGAGCGCTTGGCACTGGATGTGCTCT 360
 QY 404 GTCCATGTGTCTCAACTGAGTCAAGTGGTGGAGAGTGGGAGGAAATGATGATGTC 463
 CC GTCCATGTGTCTCAACTGAGTCAAGTGGTGGAGAGTGGGAGGAAATGATGATGTC 420
 DB 361 GTCCATGTGTCTCAACTGAGTCAAGTGGTGGAGAGTGGGAGGAAATGATGATGTC 420
 QY 464 GATCCCTGCTCATTTGGAGATGATGACATGACACCCGACCAAGGTTATGAGAGATGTGG 523
 CC GATCCCTGCTCATTTGGAGATGATGACATGACACCCGACCAAGGTTATGAGAGATGTGG 480
 DB 421 GATCCCTGCTCATTTGGAGATGATGACATGACACCCGACCAAGGTTATGAGAGATGTGG 480
 QY 524 GCGCGATGACATGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 583
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 CC ATATGAG 660
 DB 601 ATATGAG 660

QY 704 ATCCGATGCCCATATATATGATGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGTT 763
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 CC TTATGAG 745
 DB 721 TTATGAG 745

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 ID AXX98011 standard; cDNA; 1106 BP.
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 XX AXX98011;
 DT 16-MAY-2003 (first entry)
 DT 16-MAY-2003 (first entry)
 DE Human PRO polynucleotide #268.
 XX Human PRO gene; as; cytosolic; chromosome mapping; gene mapping;
 XX Human PRO gene; as; cytosolic; chromosome mapping; gene mapping;
 XX Human PRO gene; as; cytosolic; chromosome mapping; gene mapping;
 XX chondrocyte differentiation; chondrocyte proliferation; tumour.
 XX Homo sapiens.
 XX US2003032102-A1.
 XX 13-FEB-2003.
 XX 17-JUN-2002; 200208-0173697.
 XX 16-SEP-1998; 9800-US19330
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; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; REMARKS: See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 535
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-672-535

Query Match: 57.4%; Score 743.4; DB 12; Length 1106;
Best Local Similarity 99.9%; Pred. No. 4,1e-237;
Matches 744; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 TGAATCGGGAGATGGCTGGAGAGTCTGCTGGCGGTACAGAGCTTCAGCTGCC 403
DB 1 TGAATCGGGAGATGGCTGGAGAGTCTGCTGGCGGTACAGAGCTTCAGCTGCC 60
QY 104 CAGAGTCTCCCTTCACAGCGGGCCCTCTGCTGGCGGTACAGAGCTTCAGCTGCC 363
DB 61 CAGAGTCTCCCTTCACAGCGGGCCCTCTGCTGGCGGTACAGAGCTTCAGCTGCC 120
QY 164 CAGAGTCTCCCTTCACAGCGGGCCCTCTGCTGGCGGTACAGAGCTTCAGCTGCC 223
DB 121 CAGAGTCTCCCTTCACAGCGGGCCCTCTGCTGGCGGTACAGAGCTTCAGCTGCC 180
QY 224 TTTCTCTGCTGGTGGTCTTGAATGAGTGAATTCCTCCACATACAGAGCTTCGAA 283
DB 181 TTTCTCTGCTGGTGGTCTTGAATGAGTGAATTCCTCCACATACAGAGCTTCGAA 240
QY 284 TTGCACACTGTTACAACTGGACACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 343
DB 241 TTGCACACTGTTACAACTGGACACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 344 CTCTACATGCTGAATGAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 403
DB 301 CTCTACATGCTGAATGAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
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DB 361 GTCCATATGCTGAATGAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 420
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RESULT 2

US-10-187-749-535

; Sequence 535, Application US/0187749

; General Information: US/0187749

; Applicant: Baker, Kevin P.

Db 361 GTCCCTAGTGTCAACCTAGCTCAGATGCTGGCAGAGGTGGGAATGGATGATGC 420
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RESULTS

; Sequence 535, Application US/0194457
 ; Publication No. US2003015307A1
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Gudowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: San, Joon
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOT

; CURRENT INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOT

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; CURRENT INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOT

; CURRENT INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOT

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; CURRENT INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOT

; ORGANISM: Homo Sapiens
 US-10-194-457-535

Query Match 57 48, Score 715.4, DB 12, Length 1106;
 Best Local Similarity 50.98; Pval No. 4, 1e-237;
 Matches 744; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 TGAATCTGAG 103
 Db 1 TGAATCTGAG 60
 QY 104 TGAATCTGAG 163
 Db 61 TGAATCTGAG 120
 QY 164 TGAATCTGAG 223
 Db 122 TGAATCTGAG 180
 QY 224 TGAATCTGAG 283
 Db 181 TGAATCTGAG 240
 QY 284 TGAATCTGAG 343
 Db 241 TGAATCTGAG 300
 QY 344 TGAATCTGAG 403
 Db 301 TGAATCTGAG 360
 QY 404 TGAATCTGAG 463
 Db 361 TGAATCTGAG 420
 QY 464 TGAATCTGAG 523
 Db 421 TGAATCTGAG 480
 QY 524 TGAATCTGAG 583
 Db 481 TGAATCTGAG 540
 QY 584 TGAATCTGAG 643
 Db 541 TGAATCTGAG 600
 QY 644 TGAATCTGAG 703
 Db 601 TGAATCTGAG 660
 QY 704 TGAATCTGAG 763
 Db 661 TGAATCTGAG 720

RESULTS

; Sequence 535, Application US/0184642
 ; Publication No. US2003015753A1
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Gudowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: San, Joon
 ; APPLICANT: Smith, Victoria

US-10-184-542-535

; Sequence 535, Application US/0184642

; Publication No. US2003015753A1

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gurney, Austin L.

; APPLICANT: Gudowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: San, Joon

; APPLICANT: Smith, Victoria

; APPLICANT: Smith, Victoria

; APPLICANT: Smith, Victoria

; APPLICANT: Smith, Victoria

; APPLICANT: Smith, Victoria

; APPLICANT: Smith, Victoria

; APPLICANT: Smith, Victoria

; APPLICANT: Smith, Victoria

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: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SORTED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: ACIDS ENCODING THE SAME
: REFERENCE TO PUBLICATION OR OTHER DOCUMENT: US/01/84, 442
: CURRENT FILING DATE: 2002-06-27
: Prior Application removed - see file Wrapper or Palm
: SEQ ID NO 535
: LENGTH: 1106
: ORGANISM: Homo Sapien
: US-10-184-642-535

Query Match      57.4% Score 743.4; DB 32; Length 1106;
Best Local Similarity 99.9%; Pred. No. 4.1e+237;
Matches 744; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 TGGATCTGCGGAATGTGGCTGGAGAGTCTGCTGGCTGGACAGCTGCGACGCTGCGCC 103
DB 1 TGGATCTGCGGAATGTGGCTGGAGAGTCTGCTGGCTGGACAGCTGCGACGCTGCGCC 0
QY 104 CAGGACTGCTCCGACGAGCGCGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 163
DB 61 CAGGACTGCTCCGACGAGCGCGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
QY 164 CAGGACTGCTCCGACGAGCGCGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 223
DB 121 CAGGACTGCTCCGACGAGCGCGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 224 TTTCCTCTGCTGGTCTCTGTAAAGTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 283
DB 181 TTTCCTCTGCTGGTCTCTGTAAAGTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
QY 284 TTGGACAACTGTGTGAAGTGAACAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 343
DB 241 TTGGACAACTGTGTGAAGTGAACAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 344 CTGACATGCGACATGAATGTGAGACAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 403
DB 301 CTGACATGCGACATGAATGTGAGACAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 404 GTCCACAGATGTCCAACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 463
DB 361 GTCCACAGATGTCCAACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 464 GTCGCTCTGATCTGTGATGTGACATGCGCCGACGAGAGCCCTCTGTGTGTGTGTGTGTGTGT 523
DB 421 GTCGCTCTGATCTGTGATGTGACATGCGCCGACGAGAGCCCTCTGTGTGTGTGTGTGTGTGT 480
QY 524 GCGCAGACGATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 583
DB 481 GCGCAGACGATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 584 CTGATATTTTTCGAGAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643
DB 541 CTGATATTTTTCGAGAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

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: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SORTED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: ACIDS ENCODING THE SAME
: REFERENCE TO PUBLICATION OR OTHER DOCUMENT: US/01/84, 442
: CURRENT FILING DATE: 2002-06-27
: Prior Application removed - see file Wrapper or Palm
: SEQ ID NO 535
: LENGTH: 1106
: ORGANISM: Homo Sapien
: US-10-196-747-535

Query Match      57.4% Score 743.4; DB 12; Length 1106;
Best Local Similarity 99.9%; Pred. No. 4.1e+237;
Matches 744; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 TGGATCTGCGGAATGTGGCTGGAGAGTCTGCTGGCTGGACAGCTGCGACGCTGCGCC 103
DB 1 TGGATCTGCGGAATGTGGCTGGAGAGTCTGCTGGCTGGACAGCTGCGACGCTGCGCC 60
QY 104 CAGGACTGCTCCGACGAGCGCGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 163
DB 61 CAGGACTGCTCCGACGAGCGCGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 164 CAGGACTGCTCCGACGAGCGCGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 223
DB 121 CAGGACTGCTCCGACGAGCGCGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 224 TTTCCTCTGCTGGTCTCTGTAAAGTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 283
DB 181 TTTCCTCTGCTGGTCTCTGTAAAGTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
QY 284 TTGGACAACTGTGTGAAGTGAACAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 343
DB 241 TTGGACAACTGTGTGAAGTGAACAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 344 CTGACATGCGACATGAATGTGAGACAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 403
DB 301 CTGACATGCGACATGAATGTGAGACAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 404 GTCCACAGATGTCCAACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 463
DB 361 GTCCACAGATGTCCAACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 464 GTCGCTCTGATCTGTGATGTGACATGCGCCGACGAGAGCCCTCTGTGTGTGTGTGTGTGTGT 523
DB 421 GTCGCTCTGATCTGTGATGTGACATGCGCCGACGAGAGCCCTCTGTGTGTGTGTGTGTGTGT 480
QY 524 GCGCAGACGATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 583
DB 481 GCGCAGACGATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 584 CTGATATTTTTCGAGAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643
DB 541 CTGATATTTTTCGAGAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 1: 535
; LENGTH: 1106
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-173-692-535

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Query Match 57.48; Score 743.4; DB 12; Length 1106;
Best Local Similarity 59.94; Pred. No. 4.1e-237;
Matches 744; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 44 TGGATCTGGGGAATGTGGCTGGAGAGCTCTCGCTGGTCAAGCTCCAGCTGCC 103
Db 1 TGGATCTGGGGAATGTGGCTGGAGAGCTCTCGCTGGTCAAGCTCCAGCTGCC 60
QY 104 CAGAGATGCTCCCTGAGCCAGCCGCGCCGCTCTGCTGGAGAGAGCGCGAGCG 163
Db 61 CAGAGATGCTCCCTGAGCCAGCCGCGCCGCTCTGCTGGAGAGAGCGCGAGCG 120
QY 164 CAGAGCGCTGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
Db 121 CAGAGCGCTGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 224 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 283
Db 181 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 284 TTGGACAGCTGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
Db 241 TTGGACAGCTGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 344 CTCATATGTGATCAATTAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403
Db 301 CTCATATGTGATCAATTAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 404 GTGCCATAGTCAACTCAGTCAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGATG 463
Db 361 GTGCCATAGTCAACTCAGTCAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGATG 420
QY 464 GATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
Db 422 GATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 524 GCGCATGAGTCAAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
Db 481 GCGCATGAGTCAAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 584 CTGATATTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
Db 541 CTGATATTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 644 ATNAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
Db 601 ATNAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 704 ATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
Db 661 ATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 764 TTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
Db 721 TTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 745

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RESULT 10

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US-10-173-694-535
; Accession No. AG011464 Genbank US/0173694
; Publication No. 852003056107A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; INVENTOR: Baker, Kevin P.
; ATTORNEY: Dinsmoys, Luc

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hahn, Michael
; APPLICANT: Smith, Victoria
; APPLICANT: Retanabe, Orlia K.
; APPLICANT: Retanabe, William I.
; APPLICANT: Retanabe, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/010/473 654
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT FILING DATE: 2002-06-17
; Prior Application Removed - See File Wrapper or Palm
; NEW Application Number: 010/473 654
; SEQ ID NO 535
; LENGTH: 1106
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-173-694-535
Query Match 57.48; Score 743.4; DB 12; Length 1106;
Best Local Similarity 59.94; Pred. No. 4.1e-237;
Matches 744; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 44 TGGATCTGGGGAATGTGGCTGGAGAGCTCTCGCTGGTCAAGCTCCAGCTGCC 103
Db 1 TGGATCTGGGGAATGTGGCTGGAGAGCTCTCGCTGGTCAAGCTCCAGCTGCC 60
QY 104 CAGAGATGCTCCCTGAGCCAGCCGCGCCGCTCTGCTGGAGAGAGCGCGAGCG 163
Db 61 CAGAGATGCTCCCTGAGCCAGCCGCGCCGCTCTGCTGGAGAGAGCGCGAGCG 120
QY 164 CAGAGCGCTGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
Db 121 CAGAGCGCTGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 224 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 283
Db 181 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 284 TTGGACAGCTGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
Db 241 TTGGACAGCTGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 344 CTCATATGTGATCAATTAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403
Db 301 CTCATATGTGATCAATTAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 404 GTGCCATAGTCAACTCAGTCAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGATG 463
Db 361 GTGCCATAGTCAACTCAGTCAGTGGTGGAGAGAGAGAGAGAGAGAGAGAGATG 420
QY 464 GATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
Db 422 GATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 524 GCGCATGAGTCAAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
Db 481 GCGCATGAGTCAAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 584 CTGATATTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
Db 541 CTGATATTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 644 ATNAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
Db 601 ATNAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 704 ATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
Db 661 ATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

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Job time : 3114 secs